

SEQUENCE LISTING

<110> Reinhard, Christoph
Jefferson, Anne B.
Chan, Vivien W.

<120> TTK in Diagnosis and as a Therapeutic
Target in Cancer

<130> 16932.002

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<141> 2002-02-21

<150> 60/289,813

<151> 2001-02-21

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Asn Ser Gly Thr Val Asn Gln Ile Met Met Met Ala Asn Asn Pro Glu
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gac tgg ttg agt ttg ttg ctc aaa cta gag aaa aac agt gtt ccg cta 1214
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Ile Gln Val Arg Phe Ala Glu Leu Lys Ala Ile Gln Glu Pro Asp Asp
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cca cta gaa atg ctg gaa att gcc ctg cgg aat tta aac ctc caa aaa 1550
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cct Pro	gct Ala 385	gca Ala	tct Ser	tca Ser	aat Asn	cac His 390	tgg Trp	cag Gln	att Ile	ccg Pro	gag Glu 395	tta Leu	gcc Ala	cga Arg	aaa Lys	2222

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cgc aag agt tac tgg aaa aat atg tta gag gca gtt cac aca atc cat	2894
Arg Lys Ser Tyr Trp Lys Asn Met Leu Glu Ala Val His Thr Ile His	
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ttg Leu	tcg Ser	cag Gln	cag Gln	aaa Lys	tta Leu	tta Leu	gaa Glu	aat Asn	atg Met	gac Asp	gat Asp	gct Ala	caa Gln	tac Tyr	gaa Glu	1542
ttt Phe	gtc Val 505	aaa Lys	gcg Ala	caa Gln	agg Arg	aaa Lys	tta Leu	caa Gln	atg Met	gag Glu	caa Gln	caa Gln	ctt Leu	caa Gln	gaa Glu	1590
cag Gln 520	gat Asp	cag Gln	gaa Glu	gac Asp	caa Gln	gat Asp	gga Gly	aaa Lys	att Ile	caa Gln	gga Gly	ttt Phe	aaa Lys	ata Ile	ccc Pro 535	1638
gca Ala	cac His	gcc Ala	cct Pro	att Ile 540	cga Arg	tat Tyr	aca Thr	cag Gln	ccc Pro	aaa Lys	agc Ser	att Ile	gaa Glu	gca Ala	gaa Glu 550	1686
act Thr	aga Arg	gaa Glu	caa Gln	aaa Lys	ctt Leu	tta Leu	cat His	tcc Ser	aat Asn	aat Asn	act Thr	gag Glu	aat Asn	gtc Val	aag Lys	1734
agc Ser	tca Ser	aag Lys	aaa Lys	aag Lys	ggg Gly	aat Asn	ggg Gly	agg Arg	ttt Phe	tta Leu	act Thr	tta Leu	aaa Lys	cca Pro	ttg Leu	1782
cct Pro	gac Asp	agc Ser	att Ile	att Ile	caa Gln	gaa Glu	agc Ser	ctg Leu	gag Glu	att Ile	cag Gln	caa Gln	ggg Gly	gtg Val	aat Asn	1830
cca Pro 600	ttt Phe	ttc Phe	att Ile	ggg Gly	aga Arg	tcc Ser	gag Glu	gat Asp	tgc Cys	aat Asn	tgt Cys	aaa Lys	att Ile	gaa Glu	gac Asp 615	1878
aat	agg	ttg	tct	cga	gtt	cat	tgc	ttc	att	ttc	aaa	aag	agg	cat	gct	1926

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Asn Arg Leu Ser Arg Val His Cys Phe Ile Phe Lys Lys Arg His Ala
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gta ggc aaa agc atg tat gaa tct ccg gca caa ggt tta gat gat att 1974
Val Gly Lys Ser Met Tyr Glu Ser Pro Ala Gln Gly Leu Asp Asp Ile
      635                      640                      645

tgg tat tgc cac acc gga act aac gtg agc tat tta aat aat aac cgc 2022
Trp Tyr Cys His Thr Gly Thr Asn Val Ser Tyr Leu Asn Asn Asn Arg
      650                      655                      660

atg ata cag ggt acg aaa ttc ctt tta caa gac gga gat gaa atc aag 2070
Met Ile Gln Gly Thr Lys Phe Leu Leu Gln Asp Gly Asp Glu Ile Lys
      665                      670                      675

atc att tgg gat aaa aac aat aaa ttt gtc att ggc ttt aaa gtg gaa 2118
Ile Ile Trp Asp Lys Asn Asn Lys Phe Val Ile Gly Phe Lys Val Glu
      680                      685                      690                      695

att aac gat act aca ggt ctg ttt aac gag gga tta ggt atg tta caa 2166
Ile Asn Asp Thr Thr Gly Leu Phe Asn Glu Gly Leu Gly Met Leu Gln
      700                      705                      710

gaa caa aga gta gta ctt aag caa aca gcc gaa gaa aaa gat ttg gtg 2214
Glu Gln Arg Val Val Leu Lys Gln Thr Ala Glu Glu Lys Asp Leu Val
      715                      720                      725

aaa aag tta acc cag atg atg gca gct caa cgt gca aat caa ccc tcg 2262
Lys Lys Leu Thr Gln Met Met Ala Ala Gln Arg Ala Asn Gln Pro Ser
      730                      735                      740

gct tct tct tca tca atg tcg gct aag aag ccg cca gtt agc gat aca 2310
Ala Ser Ser Ser Ser Met Ser Ala Lys Lys Pro Pro Val Ser Asp Thr
      745                      750                      755

aat aat aac ggc aat aat tcg gta cta aac gac ttg gta gag tca ccg 2358
Asn Asn Asn Gly Asn Asn Ser Val Leu Asn Asp Leu Val Glu Ser Pro
      760                      765                      770                      775

att aat gcg aat acg ggg aac att ttg aag aga ata cat tcg gta agt 2406
Ile Asn Ala Asn Thr Gly Asn Ile Leu Lys Arg Ile His Ser Val Ser
      780                      785                      790

tta tcg caa tca caa att gat cct agt aag aag gtt aaa agg gca aaa 2454
Leu Ser Gln Ser Gln Ile Asp Pro Ser Lys Lys Val Lys Arg Ala Lys
      795                      800                      805

ttg gac caa acc tca aaa ggc ccc gag aat ttg caa ttt tcg taa 2499
Leu Asp Gln Thr Ser Lys Gly Pro Glu Asn Leu Gln Phe Ser *
      810                      815                      820

ccaaggacaa ataccatag aaaatgctgc cccttttttaa gagagaagat ggtagatacc 2559
aatactcaga attcccagta caaagaacca atatcgagat caataaacag tatgatgaac 2619
ttgcttttcgc aaataaaaga tatcactcag aagcaccacg taataaagga tgcagatagc 2679
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<211> 821
 <212> PRT
 <213> *Saccharomyces cerevisiae*

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			20					25					30		
Val	Cys	Arg	Val	Ile	Cys	Thr	Thr	Gly	Gln	Ile	Pro	Ile	Arg	Asp	Leu
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Ser	Ala	Asp	Ile	Ser	Gln	Val	Leu	Lys	Glu	Lys	Arg	Ser	Ile	Lys	Lys
	50					55					60				
Val	Trp	Thr	Phe	Gly	Arg	Asn	Pro	Ala	Cys	Asp	Tyr	His	Leu	Gly	Asn
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Ile	Ser	Arg	Leu	Ser	Asn	Lys	His	Phe	Gln	Ile	Leu	Leu	Gly	Glu	Asp
			85					90					95		
Gly	Asn	Leu	Leu	Leu	Asn	Asp	Ile	Ser	Thr	Asn	Gly	Thr	Trp	Leu	Asn
			100					105					110		
Gly	Gln	Lys	Val	Glu	Lys	Asn	Ser	Asn	Gln	Leu	Leu	Ser	Gln	Gly	Asp
		115					120					125			
Glu	Ile	Thr	Val	Gly	Val	Gly	Val	Glu	Ser	Asp	Ile	Leu	Ser	Leu	Val
	130					135					140				
Ile	Phe	Ile	Asn	Asp	Lys	Phe	Lys	Gln	Cys	Leu	Glu	Gln	Asn	Lys	Val
145					150					155					160
Asp	Arg	Ile	Arg	Ser	Asn	Leu	Lys	Asn	Thr	Ser	Lys	Ile	Ala	Ser	Pro
			165					170					175		
Gly	Leu	Thr	Ser	Ser	Thr	Ala	Ser	Ser	Met	Val	Ala	Asn	Lys	Thr	Gly
			180					185					190		
Ile	Phe	Lys	Asp	Phe	Ser	Ile	Ile	Asp	Glu	Val	Val	Gly	Gln	Gly	Ala
	195						200					205			
Phe	Ala	Thr	Val	Lys	Lys	Ala	Ile	Glu	Arg	Thr	Thr	Gly	Lys	Thr	Phe
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Ala	Val	Lys	Ile	Ile	Ser	Lys	Arg	Lys	Val	Ile	Gly	Asn	Met	Asp	Gly
225					230					235					240
Val	Thr	Arg	Glu	Leu	Glu	Val	Leu	Gln	Lys	Leu	Asn	His	Pro	Arg	Ile
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Val	Arg	Leu	Lys	Gly	Phe	Tyr	Glu	Asp	Thr	Glu	Ser	Tyr	Tyr	Met	Val
		260					265					270			
Met	Glu	Phe	Val	Ser	Gly	Gly	Asp	Leu	Met	Asp	Phe	Val	Ala	Ala	His
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Gly	Ala	Val	Gly	Glu	Asp	Ala	Gly	Arg	Glu	Ile	Ser	Arg	Gln	Ile	Leu
	290					295					300				
Thr	Ala	Ile	Lys	Tyr	Ile	His	Ser	Met	Gly	Ile	Ser	His	Arg	Asp	Leu
305					310					315					320
Lys	Pro	Asp	Asn	Ile	Leu	Ile	Glu	Gln	Asp	Asp	Pro	Val	Leu	Val	Lys
			325					330					335		
Ile	Thr	Asp	Phe	Gly	Leu	Ala	Lys	Val	Gln	Gly	Asn	Gly	Ser	Phe	Met
		340						345				350			
Lys	Thr	Phe	Cys	Gly	Thr	Leu	Ala	Tyr	Val	Ala	Pro	Glu	Val	Ile	Arg
		355					360				365				
Gly	Lys	Asp	Thr	Ser	Val	Ser	Pro	Asp	Glu	Tyr	Glu	Glu	Arg	Asn	Glu
	370					375					380				
Tyr	Ser	Ser	Leu	Val	Asp	Met	Trp	Ser	Met	Gly	Cys	Leu	Val	Tyr	Val
385					390					395					400
Ile	Leu	Thr	Gly	His	Leu	Pro	Phe	Ser	Gly	Ser	Thr	Gln	Asp	Gln	Leu
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<213> Homo sapiens

<220>

<221> CDS

<222> (289)...(1230)

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Met Leu Leu
1

tcc aaa atc aac tcg ctt gcc cac ctg cgc gcc gcg ccc tgc aac gac 345
Ser Lys Ile Asn Ser Leu Ala His Leu Arg Ala Ala Pro Cys Asn Asp
5 10 15

ctg cac gcc acc aag ctg gcg ccc ggc aag gag aag gag ccc ctg gag 393
Leu His Ala Thr Lys Leu Ala Pro Gly Lys Glu Lys Glu Pro Leu Glu
20 25 30 35

tcg cag tac cag gtg ggc ccg cta ctg ggc agc ggc ggc ttc ggc tcg 441
Ser Gln Tyr Gln Val Gly Pro Leu Leu Gly Ser Gly Gly Phe Gly Ser
40 45 50

gtc tac tca ggc atc cgc gtc tcc gac aac ttg ccg gtg gcc atc aaa 489
Val Tyr Ser Gly Ile Arg Val Ser Asp Asn Leu Pro Val Ala Ile Lys
55 60 65

cac gtg gag aag gac cgg att tcc gac tgg gga gag ctg cct aat ggc 537
His Val Glu Lys Asp Arg Ile Ser Asp Trp Gly Glu Leu Pro Asn Gly
70 75 80

act cga gtg ccc atg gaa gtg gtc ctg ctg aag aag gtg agc tcg ggt 585
Thr Arg Val Pro Met Glu Val Val Leu Leu Lys Lys Val Ser Ser Gly
85 90 95

ttc tcc ggc gtc att agg ctc ctg gac tgg ttc gag agg ccc gac agt 633
Phe Ser Gly Val Ile Arg Leu Leu Asp Trp Phe Glu Arg Pro Asp Ser
100 105 110 115

ttc gtc ctg atc ctg gag agg ccc gag ccg gtg caa gat ctc ttc gac 681
Phe Val Leu Ile Leu Glu Arg Pro Glu Pro Val Gln Asp Leu Phe Asp
120 125 130

ttc atc acg gaa agg gga gcc ctg caa gag gag ctc gcc cgc agc ttc 729
Phe Ile Thr Glu Arg Gly Ala Leu Gln Glu Glu Leu Ala Arg Ser Phe
135 140 145

ttc tgg cag gtg ctg gag gcc gtg cgg cac tgc cac aac tgc ggg gtg 777
Phe Trp Gln Val Leu Glu Ala Val Arg His Cys His Asn Cys Gly Val
150 155 160

ctc cac cgc gac atc aag gac gaa aac atc ctt atc gac ctc aat cgc 825
Leu His Arg Asp Ile Lys Asp Glu Asn Ile Leu Ile Asp Leu Asn Arg

165	170	175	
ggc gag ctc aag ctc atc gac ttc ggg tcg ggg gcg ctg ctc aaa gac			873
Gly Glu Leu Lys Leu Ile Asp Phe Gly Ser Gly Ala Leu Leu Lys Asp			
180	185	190	195
acc gtc tac acg gac ttc gat ggg acc cga gtg tat agc cct cca gag			921
Thr Val Tyr Thr Asp Phe Asp Gly Thr Arg Val Tyr Ser Pro Pro Glu			
	200	205	210
tgg atc cgc tac cat cgc tac cat ggc agg tcg gcg gca gtc tgg tcc			969
Trp Ile Arg Tyr His Arg Tyr His Gly Arg Ser Ala Ala Val Trp Ser			
	215	220	225
ctg ggg atc ctg ctg tat gat atg gtg tgt gga gat att cct ttc gag			1017
Leu Gly Ile Leu Leu Tyr Asp Met Val Cys Gly Asp Ile Pro Phe Glu			
	230	235	240
cat gac gaa gag atc atc agg ggc cag gtt ttc ttc agg cag agg gtc			1065
His Asp Glu Glu Ile Ile Arg Gly Gln Val Phe Phe Arg Gln Arg Val			
	245	250	255
tct tca gaa tgt cag cat ctc att aga tgg tgc ttg gcc ctg aga cca			1113
Ser Ser Glu Cys Gln His Leu Ile Arg Trp Cys Leu Ala Leu Arg Pro			
	260	265	270
tca gat agg cca acc ttc gaa gaa atc cag aac cat cca tgg atg caa			1161
Ser Asp Arg Pro Thr Phe Glu Glu Ile Gln Asn His Pro Trp Met Gln			
	280	285	290
gat gtt ctc ctg ccc cag gaa act gct gag atc cac ctc cac agc ctg			1209
Asp Val Leu Leu Pro Gln Glu Thr Ala Glu Ile His Leu His Ser Leu			
	295	300	305
tcg ccg ggg ccc agc aaa tag cagcctttct ggcaggtoct cccctctctt			1260
Ser Pro Gly Pro Ser Lys *			
310			
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gaaaagcagt tctggatggg gtgccttcca gatcctctct ggggctgtgt tttgagcagc 2460
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 35 40 45
 Phe Gly Ser Val Tyr Ser Gly Ile Arg Val Ser Asp Asn Leu Pro Val
 50 55 60
 Ala Ile Lys His Val Glu Lys Asp Arg Ile Ser Asp Trp Gly Glu Leu
 65 70 75 80
 Pro Asn Gly Thr Arg Val Pro Met Glu Val Val Leu Leu Lys Lys Val
 85 90 95
 Ser Ser Gly Phe Ser Gly Val Ile Arg Leu Leu Asp Trp Phe Glu Arg
 100 105 110
 Pro Asp Ser Phe Val Leu Ile Leu Glu Arg Pro Glu Pro Val Gln Asp
 115 120 125
 Leu Phe Asp Phe Ile Thr Glu Arg Gly Ala Leu Gln Glu Glu Leu Ala
 130 135 140
 Arg Ser Phe Phe Trp Gln Val Leu Glu Ala Val Arg His Cys His Asn
 145 150 155 160
 Cys Gly Val Leu His Arg Asp Ile Lys Asp Glu Asn Ile Leu Ile Asp
 165 170 175
 Leu Asn Arg Gly Glu Leu Lys Leu Ile Asp Phe Gly Ser Gly Ala Leu
 180 185 190
 Leu Lys Asp Thr Val Tyr Thr Asp Phe Asp Gly Thr Arg Val Tyr Ser
 195 200 205
 Pro Pro Glu Trp Ile Arg Tyr His Arg Tyr His Gly Arg Ser Ala Ala
 210 215 220
 Val Trp Ser Leu Gly Ile Leu Leu Tyr Asp Met Val Cys Gly Asp Ile
 225 230 235 240
 Pro Phe Glu His Asp Glu Glu Ile Ile Arg Gly Gln Val Phe Phe Arg
 245 250 255
 Gln Arg Val Ser Ser Glu Cys Gln His Leu Ile Arg Trp Cys Leu Ala
 260 265 270
 Leu Arg Pro Ser Asp Arg Pro Thr Phe Glu Glu Ile Gln Asn His Pro
 275 280 285
 Trp Met Gln Asp Val Leu Leu Pro Gln Glu Thr Ala Glu Ile His Leu
 290 295 300
 His Ser Leu Ser Pro Gly Pro Ser Lys
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<220>
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 tctgcaagaa tatctgtttt aaacttttca aagcaaggaa accccgtctt atatagggtta 240
 tccgcaaagg tcacattttc ttgcaaatag aagaaaaagc acccacaagc aactaacaac 300
 agtgccagag caaaactata tcctttgcat ccgatctcaa acgctgttct tatcgcatct 360
 gtcttcgtcc tttcatctgc atttaccttt tctttttcat cctctatttg ccttttccatt 420
 agtggaatt tttccagttt tttccctctg cgtcccggtg cacctgaaag gatctttcta 480
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 aaagaattac taaaaagaa gacaagggtg gctgctattg tgggtacacg tttcacagaa 660
 ctactttttc cttgtccttc tccagacatc aacgtcatac aactaaaact gataaagtac 720
 ccgtttttcc gtacatttct atagatacat tattatatta agcagatcga gacgttaatt 780
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 Met Glu Asp Lys Phe Ala Asn Leu Ser Leu His Glu Lys Thr
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 ggt aag tca tct atc caa tta aac gag caa aca ggc tca gat aat ggc 878
 Gly Lys Ser Ser Ile Gln Leu Asn Glu Gln Thr Gly Ser Asp Asn Gly
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 Ser Ala Val Lys Arg Thr Ser Ser Thr Ser Ser His Tyr Asn Asn Ile
 35 40 45
 aac gct gac ctt cat gct cgt gta aaa gct ttt caa gaa caa cgt gca 974
 Asn Ala Asp Leu His Ala Arg Val Lys Ala Phe Gln Glu Gln Arg Ala
 50 55 60
 ttg aaa agg tct gcc agc gtg ggc agt aat caa agc gag caa gac aaa 1022
 Leu Lys Arg Ser Ala Ser Val Gly Ser Asn Gln Ser Glu Gln Asp Lys
 65 70 75
 ggc agt tca caa tca cct aaa cat att cag cag att gtt aat aag cca 1070
 Gly Ser Ser Gln Ser Pro Lys His Ile Gln Gln Ile Val Asn Lys Pro
 80 85 90
 ttg ccg cct ctt ccc gta gca gga agt tct aag gtt tca caa aga atg 1118
 Leu Pro Pro Leu Pro Val Ala Gly Ser Ser Lys Val Ser Gln Arg Met
 95 100 105 110
 agt agc caa gtc gtg caa gcg tcc tcc aag agc act ctt aag aac gtt 1166
 Ser Ser Gln Val Val Gln Ala Ser Ser Lys Ser Thr Leu Lys Asn Val
 115 120 125
 ctg gac aat caa gaa aca caa aac att acc gac gta aat att aac atc 1214
 Leu Asp Asn Gln Glu Thr Gln Asn Ile Thr Asp Val Asn Ile Asn Ile
 130 135 140
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 Asp Thr Thr Lys Ile Thr Ala Thr Thr Ile Gly Val Asn Thr Gly Leu
 145 150 155

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160			165			170											
cat	aag	gcg	caa	ttg	ctg	aat	cct	aac	aga	agg	gca	cca	aga	agg	ccg	1358	
His	Lys	Ala	Gln	Leu	Leu	Asn	Pro	Asn	Arg	Arg	Ala	Pro	Arg	Arg	Pro		
175			180			185			190								
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Leu	Ser	Thr	Gln	His	Pro	Thr	Arg	Pro	Asn	Val	Ala	Pro	His	Lys	Ala		
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cct	gct	ata	atc	aac	aca	cca	aaa	caa	agt	tta	agt	gcc	cgt	cga	ggg	1454	
Pro	Ala	Ile	Ile	Asn	Thr	Pro	Lys	Gln	Ser	Leu	Ser	Ala	Arg	Arg	Gly		
			210			215			220								
ctc	aaa	tta	cca	cca	gga	gga	atg	tca	tta	aaa	atg	ccc	act	aaa	aca	1502	
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225						230			235								
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Pro	Gly	Ser	Leu	Ile	Asn	Gly	Val	Gln	Ser	Thr	Ser	Thr	Ser	Ser	Ser		
			275						280			285					
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Ser	Asn	Asn	Ser	Ser	Asn	Ser	Gly	Ser	Ser	Gly	Gly	Gly	Gly	Leu	Phe		
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gca	aat	ttc	tcg	aaa	tac	gtg	gat	atc	aaa	tcc	ggc	tct	ttg	aat	ttt	1790	
Ala	Asn	Phe	Ser	Lys	Tyr	Val	Asp	Ile	Lys	Ser	Gly	Ser	Leu	Asn	Phe		
320						325			330								
gca	ggc	aaa	cta	tcg	cta	tcc	tct	aaa	gga	ata	gat	ttc	agc	aat	ggt	1838	
Ala	Gly	Lys	Leu	Ser	Leu	Ser	Ser	Lys	Gly	Ile	Asp	Phe	Ser	Asn	Gly		
335			340						345								
tct	agt	tcg	aga	att	aca	ttg	gac	gaa	cta	gaa	ttt	ttg	gat	gaa	ctg	1886	
Ser	Ser	Ser	Arg	Ile	Thr	Leu	Asp	Glu	Leu	Glu	Phe	Leu	Asp	Glu	Leu		
			355						360			365					
ggt	cat	ggt	aac	tat	ggt	aac	gtc	tca	aag	gta	ctg	cat	aag	ccc	aca	1934	
Gly	His	Gly	Asn	Tyr	Gly	Asn	Val	Ser	Lys	Val	Leu	His	Lys	Pro	Thr		
			370			375			380								

aat	ggt	att	atg	gcg	acg	aag	gaa	gtc	cgt	ttg	gag	cta	gat	gag	gct	1982
Asn	Val	Ile	Met	Ala	Thr	Lys	Glu	Val	Arg	Leu	Glu	Leu	Asp	Glu	Ala	
		385				390				395						
aaa	ttt	aga	caa	att	tta	atg	gaa	cta	gaa	ggt	ttg	cat	aaa	tgc	aat	2030
Lys	Phe	Arg	Gln	Ile	Leu	Met	Glu	Leu	Glu	Val	Leu	His	Lys	Cys	Asn	
		400				405				410						
tct	ccc	tat	att	gtg	gat	ttt	tat	ggg	gca	ttc	ttt	att	gag	ggc	gcc	2078
Ser	Pro	Tyr	Ile	Val	Asp	Phe	Tyr	Gly	Ala	Phe	Phe	Ile	Glu	Gly	Ala	
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gtc	tac	atg	tgt	atg	gaa	tac	atg	gat	ggg	ggg	tcc	ttg	gat	aaa	ata	2126
Val	Tyr	Met	Cys	Met	Glu	Tyr	Met	Asp	Gly	Gly	Ser	Leu	Asp	Lys	Ile	
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tac	gac	gaa	tca	tct	gaa	atc	ggc	ggc	att	gat	gaa	cct	cag	cta	gcg	2174
Tyr	Asp	Glu	Ser	Ser	Glu	Ile	Gly	Gly	Ile	Asp	Glu	Pro	Gln	Leu	Ala	
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ttt	att	gcc	aat	gct	gtc	att	cat	gga	cta	aaa	gaa	ctc	aaa	gag	cag	2222
Phe	Ile	Ala	Asn	Ala	Val	Ile	His	Gly	Leu	Lys	Glu	Leu	Lys	Glu	Gln	
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cat	aat	atc	ata	cac	aga	gat	gtc	aaa	cca	aca	aat	att	tta	tgt	tca	2270
His	Asn	Ile	Ile	His	Arg	Asp	Val	Lys	Pro	Thr	Asn	Ile	Leu	Cys	Ser	
		480				485				490						
gcc	aac	caa	ggc	acc	gta	aag	ctg	tgc	gat	ttc	ggg	ggt	tct	ggg	aat	2318
Ala	Asn	Gln	Gly	Thr	Val	Lys	Leu	Cys	Asp	Phe	Gly	Val	Ser	Gly	Asn	
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ttg	gtg	gca	tct	tta	gcg	aag	act	aat	att	ggg	tgt	cag	tca	tac	atg	2366
Leu	Val	Ala	Ser	Leu	Ala	Lys	Thr	Asn	Ile	Gly	Cys	Gln	Ser	Tyr	Met	
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gca	cct	gaa	cga	atc	aaa	tcg	ttg	aat	cca	gat	aga	gcc	acc	tat	acc	2414
Ala	Pro	Glu	Arg	Ile	Lys	Ser	Leu	Asn	Pro	Asp	Arg	Ala	Thr	Tyr	Thr	
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gta	cag	tca	gac	atc	tgg	tct	tta	ggg	tta	agc	att	ctg	gaa	atg	gca	2462
Val	Gln	Ser	Asp	Ile	Trp	Ser	Leu	Gly	Leu	Ser	Ile	Leu	Glu	Met	Ala	
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cta	ggg	aga	tat	ccg	tat	cca	cca	gaa	aca	tac	gac	aac	att	ttc	tct	2510
Leu	Gly	Arg	Tyr	Pro	Tyr	Pro	Pro	Glu	Thr	Tyr	Asp	Asn	Ile	Phe	Ser	
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caa	ttg	agc	gct	att	gtt	gat	ggg	ccg	cca	ccg	aga	tta	cct	tca	gat	2558
Gln	Leu	Ser	Ala	Ile	Val	Asp	Gly	Pro	Pro	Pro	Arg	Leu	Pro	Ser	Asp	
		575		580				585						590		
aaa	ttc	agt	tct	gac	gca	caa	gat	ttt	gtt	tct	tta	tgt	cta	caa	aag	2606
Lys	Phe	Ser	Ser	Asp	Ala	Gln	Asp	Phe	Val	Ser	Leu	Cys	Leu	Gln	Lys	
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Ile Pro Glu Arg Arg Pro Thr Tyr Ala Ala Leu Thr Glu His Pro Trp
610 615 620

tta gta aaa tac aga aac cag gat gtc cac atg agt gag tat atc act 2702
Leu Val Lys Tyr Arg Asn Gln Asp Val His Met Ser Glu Tyr Ile Thr
625 630 635

gaa cga tta gaa agg cgc aac aaa atc tta cgg gaa cgt ggt gag aat 2750
Glu Arg Leu Glu Arg Arg Asn Lys Ile Leu Arg Glu Arg Gly Glu Asn
640 645 650

ggt tta tct aaa aat gta ccg gca tta cat atg ggt ggt tta tag 2795
Gly Leu Ser Lys Asn Val Pro Ala Leu His Met Gly Gly Leu *
655 660 665

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gctaggaaag aaaaaaaagt ccaaaatcat cgagaaaata aaaggtgttt tgaaagttca 3275
aatccacgtt attgagagta gatgtggagt ctggaccagg aactatacct gtatcttacc 3335
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gagctc 3401

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<213> *Saccharomyces cerevisiae*

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35 40 45
Asp Leu His Ala Arg Val Lys Ala Phe Gln Glu Gln Arg Ala Leu Lys
50 55 60
Arg Ser Ala Ser Val Gly Ser Asn Gln Ser Glu Gln Asp Lys Gly Ser
65 70 75 80
Ser Gln Ser Pro Lys His Ile Gln Gln Ile Val Asn Lys Pro Leu Pro
85 90 95
Pro Leu Pro Val Ala Gly Ser Ser Lys Val Ser Gln Arg Met Ser Ser
100 105 110
Gln Val Val Gln Ala Ser Ser Lys Ser Thr Leu Lys Asn Val Leu Asp
115 120 125
Asn Gln Glu Thr Gln Asn Ile Thr Asp Val Asn Ile Asn Ile Asp Thr
130 135 140
Thr Lys Ile Thr Ala Thr Thr Ile Gly Val Asn Thr Gly Leu Pro Ala
145 150 155 160
Thr Asp Ile Thr Pro Ser Val Ser Asn Thr Ala Ser Ala Thr His Lys
165 170 175
Ala Gln Leu Leu Asn Pro Asn Arg Arg Ala Pro Arg Arg Pro Leu Ser
180 185 190

Thr	Gln	His	Pro	Thr	Arg	Pro	Asn	Val	Ala	Pro	His	Lys	Ala	Pro	Ala	195	200	205
Ile	Ile	Asn	Thr	Pro	Lys	Gln	Ser	Leu	Ser	Ala	Arg	Arg	Gly	Leu	Lys	210	215	220
Leu	Pro	Pro	Gly	Gly	Met	Ser	Leu	Lys	Met	Pro	Thr	Lys	Thr	Ala	Gln	225	230	235
Gln	Pro	Gln	Gln	Phe	Ala	Pro	Ser	Pro	Ser	Asn	Lys	Lys	His	Ile	Glu	245	250	255
Thr	Leu	Ser	Asn	Ser	Lys	Val	Val	Glu	Gly	Lys	Arg	Ser	Asn	Pro	Gly	260	265	270
Ser	Leu	Ile	Asn	Gly	Val	Gln	Ser	Thr	Ser	Thr	Ser	Ser	Ser	Thr	Glu	275	280	285
Gly	Pro	His	Asp	Thr	Val	Gly	Thr	Thr	Pro	Arg	Thr	Gly	Asn	Ser	Asn	290	295	300
Asn	Ser	Ser	Asn	Ser	Gly	Ser	Ser	Gly	Gly	Gly	Gly	Leu	Phe	Ala	Asn	305	310	315
Phe	Ser	Lys	Tyr	Val	Asp	Ile	Lys	Ser	Gly	Ser	Leu	Asn	Phe	Ala	Gly	325	330	335
Lys	Leu	Ser	Leu	Ser	Ser	Lys	Gly	Ile	Asp	Phe	Ser	Asn	Gly	Ser	Ser	340	345	350
Ser	Arg	Ile	Thr	Leu	Asp	Glu	Leu	Glu	Phe	Leu	Asp	Glu	Leu	Gly	His	355	360	365
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Arg	Gln	Ile	Leu	Met	Glu	Leu	Glu	Val	Leu	His	Lys	Cys	Asn	Ser	Pro	405	410	415
Tyr	Ile	Val	Asp	Phe	Tyr	Gly	Ala	Phe	Phe	Ile	Glu	Gly	Ala	Val	Tyr	420	425	430
Met	Cys	Met	Glu	Tyr	Met	Asp	Gly	Gly	Ser	Leu	Asp	Lys	Ile	Tyr	Asp	435	440	445
Glu	Ser	Ser	Glu	Ile	Gly	Gly	Ile	Asp	Glu	Pro	Gln	Leu	Ala	Phe	Ile	450	455	460
Ala	Asn	Ala	Val	Ile	His	Gly	Leu	Lys	Glu	Leu	Lys	Glu	Gln	His	Asn	465	470	475
Ile	Ile	His	Arg	Asp	Val	Lys	Pro	Thr	Asn	Ile	Leu	Cys	Ser	Ala	Asn	485	490	495
Gln	Gly	Thr	Val	Lys	Leu	Cys	Asp	Phe	Gly	Val	Ser	Gly	Asn	Leu	Val	500	505	510
Ala	Ser	Leu	Ala	Lys	Thr	Asn	Ile	Gly	Cys	Gln	Ser	Tyr	Met	Ala	Pro	515	520	525
Glu	Arg	Ile	Lys	Ser	Leu	Asn	Pro	Asp	Arg	Ala	Thr	Tyr	Thr	Val	Gln	530	535	540
Ser	Asp	Ile	Trp	Ser	Leu	Gly	Leu	Ser	Ile	Leu	Glu	Met	Ala	Leu	Gly	545	550	555
Arg	Tyr	Pro	Tyr	Pro	Pro	Glu	Thr	Tyr	Asp	Asn	Ile	Phe	Ser	Gln	Leu	565	570	575
Ser	Ala	Ile	Val	Asp	Gly	Pro	Pro	Pro	Arg	Leu	Pro	Ser	Asp	Lys	Phe	580	585	590
Ser	Ser	Asp	Ala	Gln	Asp	Phe	Val	Ser	Leu	Cys	Leu	Gln	Lys	Ile	Pro	595	600	605
Glu	Arg	Arg	Pro	Thr	Tyr	Ala	Ala	Leu	Thr	Glu	His	Pro	Trp	Leu	Val	610	615	620
Lys	Tyr	Arg	Asn	Gln	Asp	Val	His	Met	Ser	Glu	Tyr	Ile	Thr	Glu	Arg	625	630	635
Leu	Glu	Arg	Arg	Asn	Lys	Ile	Leu	Arg	Glu	Arg	Gly	Glu	Asn	Gly	Leu	640		

Ser Lys Asn Val Pro Ala Leu His Met Gly Gly Leu

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<212> DNA
<213> Homo sapiens
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atg	gcg	gag	cca	gat	ctg	gag	tgc	gag	cag	atc	cgt	ctg	aag	tgt	att	168
Met	Ala	Glu	Pro	Asp	Leu	Glu	Cys	Glu	Gln	Ile	Arg	Leu	Lys	Cys	Ile	
1				5					10					15		
cgt	aag	gag	ggc	ttc	ttc	acg	gtg	cct	ccg	gaa	cac	agg	ctg	gga	cga	216
Arg	Lys	Glu	Gly	Phe	Phe	Thr	Val	Pro	Pro	Glu	His	Arg	Leu	Gly	Arg	
			20					25					30			
tgc	cgg	agt	gtg	aag	gag	ttt	gag	aag	ctg	aac	cgc	att	gga	gag	ggc	264
Cys	Arg	Ser	Val	Lys	Glu	Phe	Glu	Lys	Leu	Asn	Arg	Ile	Gly	Glu	Gly	
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acc	tac	ggc	att	gtg	tat	cgg	gcc	cgg	gac	acc	cag	aca	gat	gag	att	312
Thr	Tyr	Gly	Ile	Val	Tyr	Arg	Ala	Arg	Asp	Thr	Gln	Thr	Asp	Glu	Ile	
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gtc	gca	ctg	aag	aag	gtg	cgg	atg	gac	aag	gag	aag	gat	ggc	atc	ccc	360
Val	Ala	Leu	Lys	Lys	Val	Arg	Met	Asp	Lys	Glu	Lys	Asp	Gly	Ile	Pro	
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atc	agc	agc	ttg	cgg	gag	atc	acg	ctg	ctg	ctc	cgc	ctg	cgt	cat	ccg	408
Ile	Ser	Ser	Leu	Arg	Glu	Ile	Thr	Leu	Leu	Leu	Arg	Leu	Arg	His	Pro	
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aac	atc	gtg	gag	ctg	aag	gag	gtg	gtt	gtg	ggg	aac	cac	ctg	gag	agc	456
Asn	Ile	Val	Glu	Leu	Lys	Glu	Val	Val	Val	Gly	Asn	His	Leu	Glu	Ser	
			100					105					110			
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Ile	Phe	Leu	Val	Met	Gly	Tyr	Cys	Glu	Gln	Asp	Leu	Ala	Ser	Leu	Leu	
		115					120					125				
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Glu	Asn	Met	Pro	Thr	Pro	Phe	Ser	Glu	Ala	Gln	Val	Lys	Cys	Ile	Val	
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ctg	cag	gtg	ctc	cgg	ggc	ctc	cag	tat	ctg	cac	agg	aac	ttc	att	atc	600
Leu	Gln	Val	Leu	Arg	Gly	Leu	Gln	Tyr	Leu	His	Arg	Asn	Phe	Ile	Ile	
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His Arg Asp Leu Lys Val Ser Asn Leu Leu Met Thr Asp Lys Gly Cys	
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Val Lys Thr Ala Asp Phe Gly Leu Ala Arg Ala Tyr Gly Val Pro Val	
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aag cca atg acc ccc aag gtg gtc act ctc tgg tac cga gcc cct gaa	744
Lys Pro Met Thr Pro Lys Val Val Thr Leu Trp Tyr Arg Ala Pro Glu	
195 200 205	
ctg ctg ttg gga acc acc acg cag acc acc agc atc gac atg tgg gct	792
Leu Leu Leu Gly Thr Thr Thr Gln Thr Thr Ser Ile Asp Met Trp Ala	
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Val Gly Cys Ile Leu Ala Glu Leu Leu Ala His Arg Pro Leu Leu Pro	
225 230 235 240	
ggc act tcc gag atc cac cag atc gac ttg atc gtg cag ctg ctg ggc	888
Gly Thr Ser Glu Ile His Gln Ile Asp Leu Ile Val Gln Leu Leu Gly	
245 250 255	
acg ccc agt gag aac atc tgg ccg ggc ttt tcc aag ctg cca ctg gtc	936
Thr Pro Ser Glu Asn Ile Trp Pro Gly Phe Ser Lys Leu Pro Leu Val	
260 265 270	
ggc cag tac agc ctc cgg aag cag ccc tac aac aac ctg aag cac aag	984
Gly Gln Tyr Ser Leu Arg Lys Gln Pro Tyr Asn Asn Leu Lys His Lys	
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Phe Pro Trp Leu Ser Glu Ala Gly Leu Arg Leu Leu His Phe Leu Phe	
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atg tac gac cct aag aaa agg gcg acg gcc ggg gac tgc ctg gag agc	1080
Met Tyr Asp Pro Lys Lys Arg Ala Thr Ala Gly Asp Cys Leu Glu Ser	
305 310 315 320	
tcc tat ttc aag gag aag ccc cta ccc tgt gag ccg gag ctc atg ccg	1128
Ser Tyr Phe Lys Glu Lys Pro Leu Pro Cys Glu Pro Glu Leu Met Pro	
325 330 335	
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Thr Phe Pro His His Arg Asn Lys Arg Ala Ala Pro Ala Thr Ser Glu	
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Gly Gln Ser Lys Arg Cys Lys Pro *	
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<211> 360

<212> PRT

<213> Homo sapiens

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Cys Arg Ser Val Lys Glu Phe Glu Lys Leu Asn Arg Ile Gly Glu Gly
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Thr Tyr Gly Ile Val Tyr Arg Ala Arg Asp Thr Gln Thr Asp Glu Ile
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Val Ala Leu Lys Lys Val Arg Met Asp Lys Glu Lys Asp Gly Ile Pro
      65          70          75          80
Ile Ser Ser Leu Arg Glu Ile Thr Leu Leu Arg Leu Arg His Pro
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Asn Ile Val Glu Leu Lys Glu Val Val Val Gly Asn His Leu Glu Ser
      100          105          110
Ile Phe Leu Val Met Gly Tyr Cys Glu Gln Asp Leu Ala Ser Leu Leu
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Glu Asn Met Pro Thr Pro Phe Ser Glu Ala Gln Val Lys Cys Ile Val
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Leu Gln Val Leu Arg Gly Leu Gln Tyr Leu His Arg Asn Phe Ile Ile
      145          150          155          160
His Arg Asp Leu Lys Val Ser Asn Leu Leu Met Thr Asp Lys Gly Cys
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Val Lys Thr Ala Asp Phe Gly Leu Ala Arg Ala Tyr Gly Val Pro Val
      180          185          190
Lys Pro Met Thr Pro Lys Val Val Thr Leu Trp Tyr Arg Ala Pro Glu
      195          200          205
Leu Leu Leu Gly Thr Thr Thr Gln Thr Thr Ser Ile Asp Met Trp Ala
      210          215          220
Val Gly Cys Ile Leu Ala Glu Leu Leu Ala His Arg Pro Leu Leu Pro
      225          230          235          240
Gly Thr Ser Glu Ile His Gln Ile Asp Leu Ile Val Gln Leu Leu Gly
      245          250          255
Thr Pro Ser Glu Asn Ile Trp Pro Gly Phe Ser Lys Leu Pro Leu Val
      260          265          270
Gly Gln Tyr Ser Leu Arg Lys Gln Pro Tyr Asn Asn Leu Lys His Lys
      275          280          285
Phe Pro Trp Leu Ser Glu Ala Gly Leu Arg Leu Leu His Phe Leu Phe
      290          295          300
Met Tyr Asp Pro Lys Lys Arg Ala Thr Ala Gly Asp Cys Leu Glu Ser
      305          310          315          320
Ser Tyr Phe Lys Glu Lys Pro Leu Pro Cys Glu Pro Glu Leu Met Pro
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Thr Phe Pro His His Arg Asn Lys Arg Ala Ala Pro Ala Thr Ser Glu

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 ctttggccac tgggaggaaa a atg gcc agt gat acc cca ggt ttc tac atg 171
 Met Ala Ser Asp Thr Pro Gly Phe Tyr Met
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 Asp Lys Leu Asn Lys Tyr Arg Gln Met His Gly Val Ala Ile Thr Tyr
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 aaa gaa ctt agt act tcg gga cct cca cat gac aga agg ttt aca ttt 267
 Lys Glu Leu Ser Thr Ser Gly Pro Pro His Asp Arg Arg Phe Thr Phe
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 caa gtt tta ata gat gag aag gaa ttt gga gaa gcc aaa ggt aga tca 315
 Gln Val Leu Ile Asp Glu Lys Glu Phe Gly Glu Ala Lys Gly Arg Ser
 45 50 55
 aag acg gag gca aga aac gct gca gcc aaa tta gct gtt gat ata ctt 363
 Lys Thr Glu Ala Arg Asn Ala Ala Lys Leu Ala Val Asp Ile Leu
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 gat aac gaa aac aag gtg gat tgt cac acg agt gca tgt gag caa ggc 411
 Asp Asn Glu Asn Lys Val Asp Cys His Thr Ser Ala Cys Glu Gln Gly
 75 80 85 90
 ttg ttc gtt ggt aac tac ata ggc ctt gtc aat agc ttt gcc cag aag 459
 Leu Phe Val Gly Asn Tyr Ile Gly Leu Val Asn Ser Phe Ala Gln Lys
 95 100 105
 aaa aag ctg tct gta aat tat gaa cag tgt gag ccc aac tct gag ttg 507
 Lys Lys Leu Ser Val Asn Tyr Glu Gln Cys Glu Pro Asn Ser Glu Leu
 110 115 120
 cct caa aga ttt att tgt aaa tgc aaa att ggg cag aca atg tat ggt 555
 Pro Gln Arg Phe Ile Cys Lys Cys Lys Ile Gly Gln Thr Met Tyr Gly
 125 130 135
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 Thr Gly Ser Gly Val Thr Lys Gln Glu Ala Lys Gln Leu Ala Ala Lys
 140 145 150

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gac gcc agg ttt aac agc gat ttt gaa gac ata gaa gaa att ggc tta Asp Ala Arg Phe Asn Ser Asp Phe Glu Asp Ile Glu Glu Ile Gly Leu 235 240 245 250																891
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 Met Ser Thr Glu Leu Phe Ser Ser
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 Asp Leu Ser Asn Leu Ser Ser Gly Glu Ile Thr Ala Thr Gln Leu Thr
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 Thr Ser Ala Asp Leu Asp Glu Thr Gly His Leu Asp Ser Ser Gly Leu
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Cys Ser Ser Ser Ala Asn Lys Glu Asn Asp Asn Gly Asn Leu Val Asp
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180 185 190
Glu Leu Met Glu Phe Ser Leu Lys Asp Gln Glu Ala Lys Val Ser Arg
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Ser Gly Leu Tyr Arg Ser Pro Ser Met Pro Glu Asn Leu Asn Arg Pro
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Arg Leu Lys Gln Val Glu Lys Phe Lys Asp Asn Thr Ile Pro Asp Lys
225 230 235 240
Val Lys Lys Lys Tyr Phe Ser Gly Gln Gly Lys Leu Arg Lys Gly Leu
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Cys Leu Lys Lys Thr Val Ser Leu Cys Asp Ile Thr Ile Thr Gln Met
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Val Cys Ala Leu Pro Thr Val Ser Gly Lys His Gln Asp Leu Lys Tyr
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Lys Arg Ile Ile Ile Val Phe His Cys Glu Phe Ser Ser Glu Arg Gly
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Pro Arg Met Cys Arg Cys Leu Arg Glu Glu Asp Arg Ser Leu Asn Gln
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Arg

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Variable	Mean	SD
Age	30.5	10.2
Gender	Male	55%
Marital status	Married	65%
Education	High school	45%
Occupation	Unemployed	35%
Income	Low	75%
Health status	Good	60%
Stress level	High	50%
Life satisfaction	Low	40%
Self-esteem	Low	35%
Depression	High	65%
Anxiety	High	55%
Loneliness	High	60%
Isolation	High	50%
Helplessness	High	65%
Worry	High	55%
Overthinking	High	60%
Procrastination	High	50%
Self-doubt	High	65%
Loss of interest	High	55%
Changes in appetite	High	60%
Sleep disturbances	High	50%
Physical symptoms	High	65%
Thoughts of self-harm	High	55%
Thoughts of suicide	High	60%
Substance use	High	50%
Self-harm	High	65%
Isolation from family	High	55%
Isolation from friends	High	60%
Isolation from community	High	50%
Isolation from work	High	65%
Isolation from school	High	55%
Isolation from religious community	High	60%
Isolation from social activities	High	50%
Isolation from hobbies	High	65%
Isolation from pets	High	55%
Isolation from nature	High	60%
Isolation from travel	High	50%
Isolation from shopping	High	65%
Isolation from dining out	High	55%
Isolation from entertainment	High	60%
Isolation from sports	High	50%
Isolation from volunteering	High	65%
Isolation from community service	High	55%
Isolation from religious practices	High	60%
Isolation from social media	High	50%
Isolation from technology	High	65%
Isolation from the internet	High	55%
Isolation from mobile phones	High	60%
Isolation from email	High	50%
Isolation from social media apps	High	65%
Isolation from video games	High	55%
Isolation from streaming services	High	60%
Isolation from online shopping	High	50%
Isolation from online banking	High	65%
Isolation from online news	High	55%
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agg aca acg aag ctg ggt cct gca aag aga gcg atg act ttg aca aat			528
Arg Thr Thr Lys Leu Gly Pro Ala Lys Arg Ala Met Thr Leu Thr Asn			
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atc ttt gat gag gat gtg cct aac tct cca aac cag cca ata aat gca			576
Ile Phe Asp Glu Asp Val Pro Asn Ser Pro Asn Gln Pro Ile Asn Ala			
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Leu Pro Leu Ile Ser Gln Ile Tyr Phe Asp Lys Gln Arg Glu Glu Asn			
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Ile Pro Phe Pro Glu His Thr Ser Asn Asn Glu Lys Ile Pro Lys Ser	
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gcc att gaa tta atg aaa gca tgt ctg tac agg aac cca gac aaa aga	2112
Ala Ile Glu Leu Met Lys Ala Cys Leu Tyr Arg Asn Pro Asp Lys Arg	
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Trp Thr Val Asp Lys Val Leu Ser Ser Thr Phe Leu Gln Pro Phe Met	
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ggc tct gag aag cct cat ata tca caa gat gat ctc aat gat gtg gta	2256
Gly Ser Glu Lys Pro His Ile Ser Gln Asp Asp Leu Asn Asp Val Val	
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Leu Phe Gly Arg Tyr Leu Arg Asn Asn His Gln Thr Ser Met Thr Thr
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Arg Thr Thr Lys Leu Gly Pro Ala Lys Arg Ala Met Thr Leu Thr Asn
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Lys Glu Arg Arg Glu Asn Thr Asp Tyr Asp Ser Ile Asp Phe Gly Asp
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Leu Asn Pro Ile Gln Tyr Ile Lys Lys His Asn Leu Pro Thr Ser Asp
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Arg Gln Ala Ala Leu Arg Lys His Ser Ser Arg Glu Leu Leu Tyr Lys
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Ser Arg Ser Ser Ser Ser Ser Leu Ser Ser Asn Asn Leu Leu Ala Asn
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Val Ser Thr Gly Ser Ser Ser Ser Lys Ser Ser Ile Glu Ile Arg Arg
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Pro Ile His Lys Ile Tyr Lys Gly Ile Ser Arg Asn Lys Asp Ser Asp
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Asp Asp Ala Ile Thr Asn Glu Asn Ile Asn Ser Lys Asn Leu Glu Val
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Lys Glu Met Leu Leu Cys Ile Lys Val Val His Asp Ala Gly Ile Val
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His Ser Asp Leu Lys Pro Ala Asn Phe Val Leu Val Lys Gly Ile Leu
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      580      585      590
Asn Ile Tyr Arg Glu Thr Gln Ile Gly Thr Pro Asn Tyr Met Ala Pro
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Glu Ala Leu Val Ala Met Asn Tyr Thr Gln Asn Ser Glu Asn Gln His
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Glu Gly Asn Lys Trp Lys Val Gly Arg Pro Ser Asp Met Trp Ser Cys
625      630      635      640
Gly Cys Ile Ile Tyr Gln Met Ile Tyr Gly Lys Pro Pro Tyr Gly Ser
      645      650      655
Phe Gln Gly Gln Asn Arg Leu Leu Ala Ile Met Asn Pro Asp Val Lys
      660      665      670
Ile Pro Phe Pro Glu His Thr Ser Asn Asn Glu Lys Ile Pro Lys Ser
      675      680      685
Ala Ile Glu Leu Met Lys Ala Cys Leu Tyr Arg Asn Pro Asp Lys Arg
      690      695      700
Trp Thr Val Asp Lys Val Leu Ser Ser Thr Phe Leu Gln Pro Phe Met
705      710      715      720
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Thr Asn Ile Ala Asp Leu Val Ser Asp Ser Ser Leu Asp Glu Asp Ser
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gat Asp	acg Thr	ttg Leu	cgt Arg 60	agg Arg	cag Gln	tca Ser	agc Ser	ggc Gly 65	gca Ala	act Thr	gct Ala	tta Leu 70	gag Glu	aga Arg	ttg Leu	245
gtc Val	tca Ser	cat His 75	cct Pro	cgt Arg	act Thr	aaa Lys	aat Asn 80	ttt Phe	gat Asp	ttg Leu	caa Gln 85	gga Gly 90	aat Asn	gga Gly	gga Gly	293
caa Gln	aat Asn 90	tct Ser	gct Ala	ttg Leu	aag Lys	gaa Glu 95	gtg Val	aat Asn	act Thr	cca Pro	gca Ala 100	tat Tyr	cag Gln	tca Ser	atg Met	341
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tta Leu	tca Ser	att Ile 155	tca Ser	aga Arg	cga Arg	cga Arg	aga Arg 160	atc Ile	ggc Gly	aga Arg	att Ile 165	gga Gly	tta Leu	ggc Gly	cct Pro	533
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cag Gln	ttt Phe 250	gat Asp	cac His	gat Asp	gtt Val	gaa Glu 255	aga Arg	aga Arg	gct Ala	agt Ser	gaa Glu 260	ctt Leu	cat His	tct Ser	cgt Arg	821
cca Gln	gtc Val	acc Ser	gtt Val	ttc Ser	caa Glu	gag Val	cct Ser	cag Val	cgt Val	tct Ser	gct Val	tct Ser	caa Glu	cca Val	tat Ser	869

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caa Gln 425	atg Met	cta Leu	gag Glu	gcg Ala 430	gtc Val	cag Gln	gta Val	gtt Val	cat His	gat Asp 435	caa Gln	aat Asn	ata Ile	gtg Val	cat His 440	1349
tcg Ser	gat Asp	ttg Leu	aag Lys	ccg Pro 445	gcc Ala	aat Asn	ttc Phe	ctg Leu	ctt Leu 450	gta Val	gaa Glu	ggg Gly	aat Asn	ttg Leu 455	aag Lys	1397
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gct Ala	ttg Leu	aca Thr	gac Asp	atg Met	aat Asn	gct Ala	cac His	aca Thr	aac Asn	tct Ser	ggc Gly	gtg Val	aaa Lys	ctc Leu	gta Val	1541

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Gln	Met	Val	Tyr	Gly	Arg	Ala	Pro	Phe	Ala	His	Leu	Lys	Met	Ile	Gln					
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ccg	tta	cct	gtt	tct	ggg	cac	acc	aat	aat	gct	cat	cca	ctt	aga	ctc	1925				
Pro	Leu	Pro	Val	Ser	Gly	His	Thr	Asn	Asn	Ala	His	Pro	Leu	Arg	Leu					
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Ser	Thr	Glu	Ile	Ser	Ala	Ser	Gln	Leu	Ser	Met	Ile	Ile	Glu	Arg	Ser					
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515 520 525
Phe Ala His Leu Lys Met Ile Gln Ala Ile Ala Ala Ile Pro Asn Glu
530 535 540
Gln Tyr His Ile His Phe Pro Glu Val Ala Leu Pro Ala Asn Ala Val
545 550 555 560
Gln Glu Lys Glu Gly Ser Leu Pro Gly Val Thr Val Gly Pro Asp Leu
565 570 575
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595 600 605
Tyr Leu Thr Pro Leu Ala Lys Lys Pro Leu Pro Val Ser Gly His Thr
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Asn Asn Ala His Pro Leu Arg Leu Ser Thr Glu Ile Ser Ala Ser Gln
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Leu Ser Met Ile Ile Glu Arg Ser Val Glu Leu Ser Lys His Lys Arg
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Met Leu Ser Asn Ser Gln Gly Gln Ser Pro Pro
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gtg ccg ttc ccc gcc ccg gcc ccg ccg ccg cag ccc ccc acc cct gcc 459
Val Pro Phe Pro Ala Pro Ala Pro Pro Pro Gln Pro Pro Thr Pro Ala
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Leu Pro His Pro Pro Ala Gln Pro Pro Pro Pro Pro Pro Gln Gln Phe
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270          275          280
tat gaa ttt ccc aac cca gaa tgg tca gaa gta tca gag gaa gtg aag 1275
Tyr Glu Phe Pro Asn Pro Glu Trp Ser Glu Val Ser Glu Glu Val Lys
285          290          295

atg ctc att cgg aat ctg ctg aaa aca gag ccc acc cag aga atg acc 1323
Met Leu Ile Arg Asn Leu Leu Lys Thr Glu Pro Thr Gln Arg Met Thr
300          305          310          315

atc acc gag ttt atg aac cac cct tgg atc atg caa tca aca aag gtc 1371
Ile Thr Glu Phe Met Asn His Pro Trp Ile Met Gln Ser Thr Lys Val
320          325          330

cct caa acc cca ctg cac acc agc cgg gtc ctg aag gag gac aag gag 1419
Pro Gln Thr Pro Leu His Thr Ser Arg Val Leu Lys Glu Asp Lys Glu
335          340          345

cgg tgg gag gat gtc aag ggg tgt ctt cat gac aag aac agc gac cag 1467
Arg Trp Glu Asp Val Lys Gly Cys Leu His Asp Lys Asn Ser Asp Gln
350          355          360

gcc act tgg ctg acc agg ttg tga gcagaggatt ctgtgttctt gtccaaactc 1521
Ala Thr Trp Leu Thr Arg Leu *
365          370

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<211> 370

<212> PRT

<213> Homo sapiens

<400> 34

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Ala Gln Pro Pro Pro Pro Pro Gln Gln Phe Pro Gln Phe His Val
35          40          45
Lys Ser Gly Leu Gln Ile Lys Lys Asn Ala Ile Ile Asp Asp Tyr Lys
50          55          60
Val Thr Ser Gln Val Leu Gly Leu Gly Ile Asn Gly Lys Val Leu Gln
65          70          75          80
Ile Phe Asn Lys Arg Thr Gln Glu Lys Phe Ala Leu Lys Met Leu Gln

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 Glu Leu Phe Ser Arg Ile Gln Asp Arg Gly Asp Gln Ala Phe Thr Glu
 145 150 155 160
 Arg Glu Ala Ser Glu Ile Met Lys Ser Ile Gly Glu Ala Ile Gln Tyr
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 Leu His Ser Ile Asn Ile Ala His Arg Asp Val Lys Pro Glu Asn Leu
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 Leu Tyr Thr Ser Lys Arg Pro Asn Ala Ile Leu Lys Leu Thr Asp Phe
 195 200 205
 Gly Phe Ala Lys Glu Thr Thr Ser His Asn Ser Leu Thr Thr Pro Cys
 210 215 220
 Tyr Thr Pro Tyr Tyr Val Ala Pro Glu Val Leu Gly Pro Glu Lys Tyr
 225 230 235 240
 Asp Lys Ser Cys Asp Met Trp Ser Leu Gly Val Ile Met Tyr Ile Leu
 245 250 255
 Leu Cys Gly Tyr Pro Pro Phe Tyr Ser Asn His Gly Leu Ala Ile Ser
 260 265 270
 Pro Gly Met Lys Thr Arg Ile Arg Met Gly Gln Tyr Glu Phe Pro Asn
 275 280 285
 Pro Glu Trp Ser Glu Val Ser Glu Glu Val Lys Met Leu Ile Arg Asn
 290 295 300
 Leu Leu Lys Thr Glu Pro Thr Gln Arg Met Thr Ile Thr Glu Phe Met
 305 310 315 320
 Asn His Pro Trp Ile Met Gln Ser Thr Lys Val Pro Gln Thr Pro Leu
 325 330 335
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 Arg Leu
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 ggtgtaccag tcagtgatta agtagaacta caagttatat aggtgtatt gtttattgct 600
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 Met Tyr Tyr Gln Gln Gly Val Phe Asn

1 5

tgt gac tat tgt ata aaa aca aat ctt gat atc cag aag cac atg aag 702
 Cys Asp Tyr Cys Ile Lys Thr Asn Leu Asp Ile Gln Lys His Met Lys
 10 15 20 25

ttt gcg act ttc cac cct gcc cat ttt tgt aaa act gca gtc atc ttg 750
 Phe Ala Thr Phe His Pro Ala His Phe Cys Lys Thr Ala Val Ile Leu
 30 35 40

gac ctt tta aac aca aat ttt aaa ctc aac caa gct gtg ata agc gga 798
 Asp Leu Leu Asn Thr Asn Phe Lys Leu Asn Gln Ala Val Ile Ser Gly .
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 Met Val Thr Val Tyr Thr Val Val Cys Phe *
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 Lys Leu Asn Gln Ala Val Ile Ser Gly Met Val Thr Val Tyr Thr Val
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          Met Gly Ile Pro Met Gly Lys Ser Met Leu Val Leu Leu
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acc ttc ttg gcc ttc gcc tcg tgc tgc att gct gct tac cgc ccc agt 639
Thr Phe Leu Ala Phe Ala Ser Cys Cys Ile Ala Ala Tyr Arg Pro Ser
      15                20                25

gag acc ctg tgc ggc ggg gag ctg gtg gac acc ctc cag ttc gtc tgt 687
Glu Thr Leu Cys Gly Gly Glu Leu Val Asp Thr Leu Gln Phe Val Cys
      30                35                40                45

ggg gac cgc ggc ttc tac ttc agc agg ccc gca agc cgt gtg agc cgt 735
Gly Asp Arg Gly Phe Tyr Phe Ser Arg Pro Ala Ser Arg Val Ser Arg
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cgc agc cgt ggc atc gtt gag gag tgc tgt ttc cgc agc tgt gac ctg 783
Arg Ser Arg Gly Ile Val Glu Glu Cys Cys Phe Arg Ser Cys Asp Leu
                65                70                75

gcc ctc ctg gag acg tac tgt gct acc ccc gcc aag tcc gag agg gac 831
Ala Leu Leu Glu Thr Tyr Cys Ala Thr Pro Ala Lys Ser Glu Arg Asp
                80                85                90

gtg tcg acc cct ccg acc gtg ctt ccg gac aac ttc ccc aga tac ccc 879
Val Ser Thr Pro Pro Thr Val Leu Pro Asp Asn Phe Pro Arg Tyr Pro
                95                100                105

gtg ggc aag ttc ttc caa tat gac acc tgg aag cag tcc acc cag cgc 927
Val Gly Lys Phe Phe Gln Tyr Asp Thr Trp Lys Gln Ser Thr Gln Arg
                110                115                120                125

ctg cgc agg ggc ctg cct gcc ctc ctg cgt gcc cgc cgg ggt cac gtg 975
Leu Arg Arg Gly Leu Pro Ala Leu Leu Arg Ala Arg Arg Gly His Val
                130                135                140

ctc gcc aag gag ctc gag gcg ttc agg gag gcc aaa cgt cac cgt ccc 1023
Leu Ala Lys Glu Leu Glu Ala Phe Arg Glu Ala Lys Arg His Arg Pro
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ctg att gct cta ccc acc caa gac ccc gcc cac ggg ggc gcc ccc cca 1071
Leu Ile Ala Leu Pro Thr Gln Asp Pro Ala His Gly Gly Ala Pro Pro
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Glu Met Ala Ser Asn Arg Lys *
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 35 40 45
 Gly Phe Tyr Phe Ser Arg Pro Ala Ser Arg Val Ser Arg Arg Ser Arg
 50 55 60
 Gly Ile Val Glu Glu Cys Cys Phe Arg Ser Cys Asp Leu Ala Leu Leu
 65 70 75 80
 Glu Thr Tyr Cys Ala Thr Pro Ala Lys Ser Glu Arg Asp Val Ser Thr
 85 90 95
 Pro Pro Thr Val Leu Pro Asp Asn Phe Pro Arg Tyr Pro Val Gly Lys
 100 105 110
 Phe Phe Gln Tyr Asp Thr Trp Lys Gln Ser Thr Gln Arg Leu Arg Arg
 115 120 125
 Gly Leu Pro Ala Leu Leu Arg Ala Arg Arg Gly His Val Leu Ala Lys
 130 135 140
 Glu Leu Glu Ala Phe Arg Glu Ala Lys Arg His Arg Pro Leu Ile Ala
 145 150 155 160
 Leu Pro Thr Gln Asp Pro Ala His Gly Gly Ala Pro Pro Glu Met Ala
 165 170 175
 Ser Asn Arg Lys
 180